

IN THE CLAIMS:

Please amend the claims as shown below.

1. (Currently Amended) A probe carrier for simultaneous quantification of two or more genes in a solution, the probe carrier having a surface on which probes capable of specifically binding to respective ones of the genes are immobilized at known locations, wherein two or more areas containing respective ones of the probes exist as separated spots on the probe carrier, wherein each of the spots was formed by ejecting a corresponding probe solution such that the respective probe solutions have the same concentration and the respective spots have a uniform diameter, and wherein the number of spots for the genes differs depending on the genes.

2 to 8. (Cancelled)

9. (Previously Presented) The probe carrier according to claim 1, wherein the amount of probe molecules per spot is the same for the same probe and different between probes having different sequences.

10. (Previously Presented) The probe carrier according to claim 1, wherein the spots are formed by an ink jet method.

11. (Previously Presented) The probe carrier according to claim 1, wherein the number of spots for respective target substances differs 100 to 1000 times between a

maximum number of spots and a minimum number of spots.

12 to 21. (Cancelled)

22. (Previously Presented) The probe carrier according to claim 1, wherein the number of spots for a target substance corresponding to a gene expected to exist at a higher ratio is larger than the number of spots for a target substance corresponding to a gene expected to exist at a lower ratio, based on expected amounts of the target substances in the solution.

23. (Previously Presented) The probe carrier according to claim 1, wherein the amount of probes immobilized per spot is known.

24. (Previously Presented) The probe carrier according to claim 22, wherein the number of probe molecules per spot is practically equal among all kinds of probes.

25. (Previously Presented) The probe carrier according to claim 23, wherein the number of spots in each of the areas is proportional to an average amount of expression, in a human, of a target gene having a sequence complementary to a respective one of the probes.